



## SEQUENCE LISTING

RECEIVED  
MAR 08 2002  
TECH CENTER 1600,2900

<100> TAKEDA, Masatoshi  
TAKEDA, Junji

<120> Gene Mutant Animals

<130> P19743

<140> 09/581,528

<141> 1999-01-07

<150> PCT/JP99/00015

<151> 1999-01-07

<160> 18

<170> PatentIn version 3.0

<210> 1

<211> 467

<212> PRT

<213> Human

<400> 1

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Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu  
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu  
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys  
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val  
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln  
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg

115		120		125
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val				
130		135		140
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys				
145		150		155
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe				
		165		170
				175
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala				
		180		185
				190
Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val				
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Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala				
		210		215
				220
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr				
		225		230
				235
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr				
		245		250
				255
Asp Leu Asp Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val				
		260		265
				270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr				
		275		280
				285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu				
		290		295
				300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr				
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				315
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe				
		325		330
				335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg				
		340		345
				350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile				
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Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly				

370

375

380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
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Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile  
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Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu  
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Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala  
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Phe Tyr Ile  
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agacggagcc ttggccaccc tgagccatta tctaattggac gaccccaggg taactcccgg  
 180

caggtggtgg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag  
 240

catgtgatca tgetctttgt ccctgtgact ctctgcatgg tggtgggtcgt ggctactatt  
 300

aagtcagtca gcttttatac ccggaaggat gggcagctaa tctatacccc attcacagaa  
 360

gataccgaga ctgtgggcca gagagccctg cactcaattc tgaatgctgc catcatgatc  
 420

agtgtcattg ttgtcatgac taccctcctg gtggttctgt ataaatacag gtgctataag

480

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ctgatctgga attttgggtgt ggtgggaatg atttccattc actggaaagg tccacttcga  
660

ctccagcagg catatctcat tatgattagt gccctcatgg ccttgggtgtt tatcaagtaa  
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960

gaaagggagt cacaagacac tgttgccagag aatgatgatg gcgggttcag tgaggaatgg  
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gaagcccaga gggacagtca tctagggcct catcgtctca cacctgagtc acgagctgct  
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gtccaggaac tttccagcag tatcctcgct ggtgaagacc cagaggaaag gggagtataa  
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agtggagact ggaacacaac catagcctgt ttcgtagcca tattaattgg tttgtgcctt  
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acattattac tccttgccat tttcaagaaa gcattgccag ctcttccaat ctccatcacc  
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Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser  
 20 25 30

Glu Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu  
 35 40 45

Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu  
 50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys  
 65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val  
 85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln  
 100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg  
 115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val  
 130 135 140

Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys  
 145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe  
 165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala  
 180 185 190

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val  
 195 200 205

Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala  
 210 215 220  
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr  
 225 230 235 240  
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr  
 245 250 255  
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val  
 260 265 270  
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr  
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 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu  
 290 295 300  
 Ala Glu Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala  
 305 310 315 320  
 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe  
 325 330 335  
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg  
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 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile  
 355 360 365  
 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly  
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 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala  
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 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile  
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 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu  
 420 425 430  
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala  
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660

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720

ctccccgaat ggaccgcatg gctcatcttg gctgtgattt cagtatatga tttgggtggct  
780

gttttatgtc ccaaaggccc acttcgtatg ctggttgaaa cagctcagga aagaaatgag  
840

actctctttc cagctcttat ctattcctca acaatgggtg ggttggtgaa tatggctgaa  
900

ggagaccag aagcccaaag gagggtagcc aagaaccca agtataacac acaaagagcg  
960

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1020

gaggcccaaa gagacagtca cctggggcct catcgctcca ctcccgagtc aagagctgct  
1080

gtccaggaac tttctgggag cattctaacg agtgaagacc cggaggaaag aggagtaaaa  
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agtggagact ggaacacaac catagcctgc tttgtagcca tactgatcgg cctgtgcctt  
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acattactcc tgctcgccat tttcaagaaa gcgttgccag cctcccccat ctccatcacc  
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<222> (1)..(18)

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<210> 10

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<210> 14  
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<220>  
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<222> (1)..(30)

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<210> 16

<211> 30  
<212> DNA  
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<220>  
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<210> 17  
<211> 30  
<212> DNA  
<213> synthetic construct

<220>  
<221> Primer  
<222> (1)..(30)

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*core*  
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<210> 18  
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<212> DNA  
<213> synthetic construct

<220>  
<221> Sequence around amino acid 213  
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<223> Sequence showing mutation at amino acid 213 of Presenilin-1

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